SEQUENCE LISTING

(1) GENERAL INFORMATION:

   (i) APPLICANT: Goodman, Corey S.

              Kidd, Thomas

              Mitchell, Kevin

              Tear, Guy

   (ii) TITLE OF INVENTION: Robo: A Novel Family of Polypeptide and
       Nucleic Acids

  (iii) NUMBER OF SEQUENCES: 12

   (iv) CORRESPONDENCE ADDRESS:

      (A) ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

      (B) STREET: 75 DENISE DRIVE

      (C) CITY: HILLSBOROUGH

      (D) STATE: CALIFORNIA

      (E) COUNTRY: USA

      (F) ZIP: 94010

    (v) COMPUTER READABLE FORM:

      (A) MEDIUM TYPE: Floppy disk

      (B) COMPUTER: IBM PC compatible

      (C) OPERATING SYSTEM: PC-DOS/MS-DOS

      (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

   (vi) CURRENT APPLICATION DATA:

      (A) APPLICATION NUMBER:

      (B) FILING DATE:

      (C) CLASSIFICATION:

  (viii) ATTORNEY/AGENT INFORMATION:

      (A) NAME: OSMAN, RICHARD A

      (B) REGISTRATION NUMBER: 36,627

      (C) REFERENCE/DOCKET NUMBER: B98-006

   (ix) TELECOMMUNICATION INFORMATION:

      (A) TELEPHONE: (650) 343-4341

      (B) TELEFAX: (650) 343-4342

(2) INFORMATION FOR SEQ ID NO:1:

   (i) SEQUENCE CHARACTERISTICS:

      (A) LENGTH: 4188 base pairs

      (B) TYPE: nucleic acid

      (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: cDNA

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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CATCCCACGG ATCTGGTCGT TAAGAAGAAT GAACCCGCCA CGCTCAACTG CAAAGTGGAG     240

GGCAAGCCGG AACCCACCAT TGAGTGGTTT AAGGATGGCG AACCCGTCAG CACCAACGAA     300

AAGAAATCGC ACCGCGTCCA GTTCAAGGAC GGCGCCCTCT TCTTTTACAG GACAATGCAA     360

GGCAAGAAGG AGCAGGACGG CGGAGAGTAC TGGTGCGTGG CCAAGAACCG AGTGGGCCAG     420

GCCGTTAGTC GCCATGCCTC CCTCCAGATA GCTGTTTTGC GCGACGATTT TCGCGTGGAG     480

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GGCATTCCAG AGCCAACGCT GATTTGGATA AAGGACGGCG TTCCCTTGGA CGACCTGAAA     600

GCCATGTCGT TTGGCGCCAG CTCCCGCGTT CGAATTGTGG ACGGTGGCAA CCTGCTGATC     660

AGCAATGTGG AGCCCATTGA TGAGGGCAAC TACAAGTGCA TTGCCCAGAA TCTGGTAGGC     720

ACCCGCGAGA GCAGCTATGC CAAGCTGATT GTCCAGGTCA AACCATACTT TATGAAGGAG     780

CCCAAGGATC AGGTGATGCT CTACGGCCAG ACAGCCACTT TCCACTGCTC AGTGGGCGGT     840

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CGGGCAGCTG ATCCTAGCAC TTATCCTGCT CCTCCAGGAA CACCTAAAGT CCTGAATGTC    1680

AGTCGCACCA GCATTAGTCT TCGTTGGGCT AAAAGCCAAG AGAAACCCGG AGCTGTGGGC    1740

CCAATCATTG GATACACTGT AGAGTACTTC AGTCCGGATC TGCAAACTGG TTGGATTGTG    1800

GCTGCCCATC GAGTCGGCGA CACTCAAGTC ACTATCTCGG GTCTCACTCC TGGCACTTCG    1860

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GCTCGAACTT TGCTGACAGG AAAGTCGGTG GAGCTAATAG ATGCCTCGGC TATCAATGCT    2040

AGTGCCGTTA GACTTGAGTG GATGCTCCAC GTGAGCGCTG ATGAGAAATA CGTAGAGGGC    2100
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ATGGATGCCT CTGCAGAATC GTTTGTGGTG GGAAACCTTA AGAAGTACAC CAAGTATGAG    2220
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CTCACCTATG AAGATGTTCC CTCCGCACCA CCGGATAACA TTCAGATTGG CATGTACAAC    2340
CAAACAGCCG GTTGGGTGCG TTGGACTCCG CCACCCTCCC AGCACCACAA TGGCAATTTG    2400
TATGGCTACA AGATTGAGGT CAGCGCCGGT AACACCATGA AGGTGCTGGC CAATATGACT    2460
CTTAATGCTA CCACCACATC TGTGCTCCTA AATAACCTAA CCACCGGAGC TGTGTACAGC    2520
GTGAGGTTGA ACTCCTTTAC CAAGGCAGGA GATGGACCTT ACTCCAAACC GATATCACTA    2580
TTCATGGACC CCACCCATCA TGTGCATCCG CCACGGGCAC ATCCAAGCGG CACCCATGAT    2640
GGGCGACATG AGGGACAGGA TCTCACGTAT CATAACAATG GCAACATACC ACCTGGCGAC    2700
ATTAATCCCA CCACTCATAA AAAGACCACT GACTACCTAT CTGGACCGTG GCTAATGGTG    2760
CTGGTCTGCA TCGTTCTTCT AGTCCTGGTT ATTTCGGCGG CTATTTCGAT GGTCTACTTC    2820
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ATAACCGCAT TAAATATCAA TAGCAAAGAG AGCCTTTGGA TAGACCATCA TCGTGGATGG    2940
CGAACTGCCG ATACTGACAA AGACTCAGGA TTAAGCGAAT CGAAGCTACT ATCCCACGTT    3000
AACAGCAGTC AATCCAACTA CAATAACTCC GATGGAGGAA CCGATTATGC AGAAGTTGAC    3060
ACCCGTAACC TTACCACCTT CTACAATTGT CGCAAGAGCC CCGATAATCC CACGCCGTAC    3120
GCCACCACTA TGATCATTGG TACCTCTTCC AGTGAGACCT GCACCAAGAC AACATCTATA    3180
AGTGCCGATA AGGACTCGGG AACTCATTCG CCCTATTCTG ACGCATTTGC CGGTCAGGTG    3240
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TCAGAGTTTC TACCCCCGCC GCCAGAACAC CCACCTCCGT CTTCTACCTA TGGATACGCA    3360
CAAGGATCTC CTGAATCTTC GCGGAAGAGC TCCAAAAGCG CAGGTTCCGG CATTTCTACA    3420
AATCAAAGCA TTCTGAACGC ATCCATACAC AGCAGCTCCT CGGGCGGCTT TTCAGCTTGG    3480
GGAGTATCGC CCCAATATGC TGTCGCCTGT CCACCGGAAA ACGTTTATAG CAATCCGCTG    3540
TCGGCAGTGG CTGGCGGCAC CCAGAACCGC TATCAGATAA CGCCCACAAA CCAACATCCG    3600
CCACAGTTAC CGGCCTACTT TGCCACCACG GGTCCAGGAG GAGCTGTACC ACCCAACCAC    3660
CTGCCATTTG CCACACAGCG TCATGCAGCC AGCGAGTACC AGGCTGGACT GAATGCAGCG    3720
CGATGTGCCC AAAGCCGCGC CTGCAACAGC TGCGATGCCT TGGCCACACC CTCGCCCATG    3780
CAACCCCCAC CGCCAGTTCC CGTACCCGAG GGCTGGTACC AACCGGTGCA TCCCAATAGC    3840
CACCCGATGC ACCCGACCTC CTCCAACCAC CAGATCTACC AGTGCTCCTC CGAGTGCTCG    3900
GATCACTCGA GGAGCTCGCA GAGTCACAAG CGGCAGCTGC AGCTCGAGGA GCACGGCAGC    3960
AGTGCCAAAC AACGCGGAGG ACACCACCGT CGACGAGCCC CGGTGGTGCA GCCGTGCATG    4020
GAGAGCGAGA ACGAGAACAT GCTGGCGGAG TACGAGCAGC GCCAGTACAC CAGCGATTGC    4080
TGCAATAGCT CCCGCGAGGG CGACACCTGC TCCTGCAGCG AGGGATCCTG TCTTTACGCC    4140
GAGGCGGGCG AGCCGGCGCC TCGTCAAATG ACTGCTAAGA ACACCTAA              4188
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(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 1395 amino acids.

          (B) TYPE: amino acid

          (C) STRANDEDNESS: single

          (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met His Pro Met His Pro Glu Asn His Ala Ile Ala Arg Ser Thr Ser
1               5                   10                  15

Thr Thr Asn Asn Pro Ser Arg Ser Arg Ser Ser Arg Met Trp Leu Leu
            20                  25                  30

Pro Ala Trp Leu Leu Leu Val Leu Val Ala Ser Asn Gly Leu Pro Ala
            35                  40                  45

Val Arg Gly Gln Tyr Gln Ser Pro Arg Ile Ile Glu His Pro Thr Asp
    50                  55                  60

Leu Val Val Lys Lys Asn Glu Pro Ala Thr Leu Asn Cys Lys Val Glu
65                  70                  75                  80

Gly Lys Pro Glu Pro Thr Ile Glu Trp Phe Lys Asp Gly Glu Pro Val
            85                  90                  95

Ser Thr Asn Glu Lys Lys Ser His Arg Val Gln Phe Lys Asp Gly Ala
            100                 105                 110

Leu Phe Phe Tyr Arg Thr Met Gln Gly Lys Lys Glu Gln Asp Gly Gly
            115                 120                 125

Glu Tyr Trp Cys Val Ala Lys Asn Arg Val Gly Gln Ala Val Ser Arg
    130                 135                 140

His Ala Ser Leu Gln Ile Ala Val Leu Arg Asp Asp Phe Arg Val Glu
145                 150                 155                 160

Pro Lys Asp Thr Arg Val Ala Lys Gly Glu Thr Ala Leu Leu Glu Cys
                165                 170                 175

Gly Pro Pro Lys Gly Ile Pro Glu Pro Thr Leu Ile Trp Ile Lys Asp
                180                 185                 190

Gly Val Pro Leu Asp Asp Leu Lys Ala Met Ser Phe Gly Ala Ser Ser
                195                 200                 205

Arg Val Arg Ile Val Asp Gly Gly Asn Leu Leu Ile Ser Asn Val Glu
    210                 215                 220

Pro Ile Asp Glu Gly Asn Tyr Lys Cys Ile Ala Gln Asn Leu Val Gly
225                 230                 235                 240

Thr Arg Glu Ser Ser Tyr Ala Lys Leu Ile Val Gln Val Lys Pro Tyr
            245                 250                 255
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Phe Met Lys Glu Pro Lys Asp Gln Val Met Leu Tyr Gly Gln Thr Ala
            260                 265                 270

Thr Phe His Cys Ser Val Gly Gly Asp Pro Pro Pro Lys Val Leu Trp
            275                 280                 285

Lys Lys Glu Glu Gly Asn Ile Pro Val Ser Arg Ala Arg Ile Leu His
            290                 295                 300

Asp Glu Lys Ser Leu Glu Ile Ser Asn Ile Thr Pro Thr Asp Glu Gly
305                 310                 315                 320

Thr Tyr Val Cys Glu Ala His Asn Asn Val Gly Gln Ile Ser Ala Arg
            325                 330                 335

Ala Ser Leu Ile Val His Ala Pro Pro Asn Phe Thr Lys Arg Pro Ser
            340                 345                 350

Asn Lys Lys Val Gly Leu Asn Gly Val Val Gln Leu Pro Cys Met Ala
            355                 360                 365

Ser Gly Asn Pro Pro Pro Ser Val Phe Trp Thr Lys Glu Gly Val Ser
            370                 375                 380

Thr Leu Met Phe Pro Asn Ser Ser His Gly Arg Gln Tyr Val Ala Ala
385                 390                 395                 400

Asp Gly Thr Leu Gln Ile Thr Asp Val Arg Gln Glu Asp Glu Gly Tyr
                405                 410                 415

Tyr Val Cys Ser Ala Phe Ser Val Val Asp Ser Ser Thr Val Arg Val
            420                 425                 430

Phe Leu Gln Val Ser Ser Val Asp Glu Arg Pro Pro Pro Ile Ile Gln
            435                 440                 445

Ile Gly Pro Ala Asn Gln Thr Leu Pro Lys Gly Ser Val Ala Thr Leu
            450                 455                 460

Pro Cys Arg Ala Thr Gly Asn Pro Ser Pro Arg Ile Lys Trp Phe His
465                 470                 475                 480

Asp Gly His Ala Val Gln Ala Gly Asn Arg Tyr Ser Ile Ile Gln Gly
                485                 490                 495

Ser Ser Leu Arg Val Asp Asp Leu Gln Leu Ser Asp Ser Gly Thr Tyr
                500                 505                 510

Thr Cys Thr Ala Ser Gly Glu Arg Gly Glu Thr Ser Trp Ala Ala Thr
            515                 520                 525

Leu Thr Val Glu Lys Pro Gly Ser Thr Ser Leu His Arg Ala Ala Asp
            530                 535                 540

Pro Ser Thr Tyr Pro Ala Pro Pro Gly Thr Pro Lys Val Leu Asn Val
545                 550                 555                 560
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Ser Arg Thr Ser Ile Ser Leu Arg Trp Ala Lys Ser Gln Glu Lys Pro
           565   570   575

Gly Ala Val Gly Pro Ile Ile Gly Tyr Thr Val Glu Tyr Phe Ser Pro
           580   585   590

Asp Leu Gln Thr Gly Trp Ile Val Ala Ala His Arg Val Gly Asp Thr
       595   600   605

Gln Val Thr Ile Ser Gly Leu Thr Pro Gly Thr Ser Tyr Val Phe Leu
       610   615   620

Val Arg Ala Glu Asn Thr Gln Gly Ile Ser Val Pro Ser Gly Leu Ser
625   630   635   640

Asn Val Ile Lys Thr Ile Glu Ala Asp Phe Asp Ala Ala Ser Ala Asn
           645   650   655

Asp Leu Ser Ala Ala Arg Thr Leu Leu Thr Gly Lys Ser Val Glu Leu
           660   665   670

Ile Asp Ala Ser Ala Ile Asn Ala Ser Ala Val Arg Leu Glu Trp Met
           675   680   685

Leu His Val Ser Ala Asp Glu Lys Tyr Val Glu Gly Leu Arg Ile His
       690   695   700

Tyr Lys Asp Ala Ser Val Pro Ser Ala Gln Tyr His Ser Ile Thr Val
705   710   715   720

Met Asp Ala Ser Ala Glu Ser Phe Val Val Gly Asn Leu Lys Lys Tyr
           725   730   735

Thr Lys Tyr Glu Phe Phe Leu Thr Pro Phe Phe Glu Thr Ile Glu Gly
           740   745   750

Gln Pro Ser Asn Ser Lys Thr Ala Leu Thr Tyr Glu Asp Val Pro Ser
           755   760   765

Ala Pro Pro Asp Asn Ile Gln Ile Gly Met Tyr Asn Gln Thr Ala Gly
       770   775   780

Trp Val Arg Trp Thr Pro Pro Ser Gln His His Asn Gly Asn Leu
785   790   795   800

Tyr Gly Tyr Lys Ile Glu Val Ser Ala Gly Asn Thr Met Lys Val Leu
           805   810   815

Ala Asn Met Thr Leu Asn Ala Thr Thr Thr Ser Val Leu Leu Asn Asn
           820   825   830

Leu Thr Thr Gly Ala Val Tyr Ser Val Arg Leu Asn Ser Phe Thr Lys
           835   840   845

Ala Gly Asp Gly Pro Tyr Ser Lys Pro Ile Ser Leu Phe Met Asp Pro
       850   855   860

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Thr His His Val His Pro Pro Arg Ala His Pro Ser Gly Thr His Asp
865   870   875   880

Gly Arg His Glu Gly Gln Asp Leu Thr Tyr His Asn Asn Gly Asn Ile
                885   890   895

Pro Pro Gly Asp Ile Asn Pro Thr Thr His Lys Lys Thr Thr Asp Tyr
                900   905   910

Leu Ser Gly Pro Trp Leu Met Val Leu Val Cys Ile Val Leu Leu Val
                915   920   925

Leu Val Ile Ser Ala Ala Ile Ser Met Val Tyr Phe Lys Arg Lys His
           930   935   940

Gln Met Thr Lys Glu Leu Gly His Leu Ser Val Val Ser Asp Asn Glu
945   950   955   960

Ile Thr Ala Leu Asn Ile Asn Ser Lys Glu Ser Leu Trp Ile Asp His
                965   970   975

His Arg Gly Trp Arg Thr Ala Asp Thr Asp Lys Asp Ser Gly Leu Ser
                980   985   990

Glu Ser Lys Leu Leu Ser His Val Asn Ser Ser Gln Ser Asn Tyr Asn
           995   1000   1005

Asn Ser Asp Gly Gly Thr Asp Tyr Ala Glu Val Asp Thr Arg Asn Leu
      1010   1015   1020

Thr Thr Phe Tyr Asn Cys Arg Lys Ser Pro Asp Asn Pro Thr Pro Tyr
1025   1030   1035   1040

Ala Thr Thr Met Ile Ile Gly Thr Ser Ser Ser Glu Thr Cys Thr Lys
                1045   1050   1055

Thr Thr Ser Ile Ser Ala Asp Lys Asp Ser Gly Thr His Ser Pro Tyr
           1060   1065   1070

Ser Asp Ala Phe Ala Gly Gln Val Pro Ala Val Pro Val Val Lys Ser
           1075   1080   1085

Asn Tyr Leu Gln Tyr Pro Val Glu Pro Ile Asn Trp Ser Glu Phe Leu
      1090   1095   1100

Pro Pro Pro Pro Glu His Pro Pro Pro Ser Ser Thr Tyr Gly Tyr Ala
1105   1110   1115   1120

Gln Gly Ser Pro Glu Ser Ser Arg Lys Ser Ser Lys Ser Ala Gly Ser
                1125   1130   1135

Gly Ile Ser Thr Asn Gln Ser Ile Leu Asn Ala Ser Ile His Ser Ser
           1140   1145   1150

Ser Ser Gly Gly Phe Ser Ala Trp Gly Val Ser Pro Gln Tyr Ala Val
           1155   1160   1165

```
Ala Cys Pro Pro Glu Asn Val Tyr Ser Asn Pro Leu Ser Ala Val Ala
    1170                1175                1180
Gly Gly Thr Gln Asn Arg Tyr Gln Ile Thr Pro Thr Asn Gln His Pro
1185                1190                1195                1200
Pro Gln Leu Pro Ala Tyr Phe Ala Thr Thr Gly Pro Gly Gly Ala Val
                1205                1210                1215
Pro Pro Asn His Leu Pro Phe Ala Thr Gln Arg His Ala Ala Ser Glu
                1220                1225                1230
Tyr Gln Ala Gly Leu Asn Ala Ala Arg Cys Ala Gln Ser Arg Ala Cys
            1235                1240                1245
Asn Ser Cys Asp Ala Leu Ala Thr Pro Ser Pro Met Gln Pro Pro Pro
    1250                1255                1260
Pro Val Pro Val Pro Glu Gly Trp Tyr Gln Pro Val His Pro Asn Ser
1265                1270                1275                1280
His Pro Met His Pro Thr Ser Ser Asn His Gln Ile Tyr Gln Cys Ser
                1285                1290                1295
Ser Glu Cys Ser Asp His Ser Arg Ser Ser Gln Ser His Lys Arg Gln
            1300                1305                1310
Leu Gln Leu Glu Glu His Gly Ser Ser Ala Lys Gln Arg Gly Gly His
            1315                1320                1325
His Arg Arg Arg Ala Pro Val Val Gln Pro Cys Met Glu Ser Glu Asn
    1330                1335                1340
Glu Asn Met Leu Ala Glu Tyr Glu Gln Arg Gln Tyr Thr Ser Asp Cys
1345                1350                1355                1360
Cys Asn Ser Ser Arg Glu Gly Asp Thr Cys Ser Cys Ser Glu Gly Ser
                1365                1370                1375
Cys Leu Tyr Ala Glu Ala Gly Glu Pro Ala Pro Arg Gln Met Thr Ala
                1380                1385                1390
Lys Asn Thr
    1395


(2) INFORMATION FOR SEQ ID NO:3:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4146 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: cDNA
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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GGTGAAAATC CACGCATCAT CGAGCATCCC ATGGACACGA CGGTGCCAAA AAATGATCCA       60
TTTACGTTTA ATTGCCAGGC CGAGGGCAAT CCAACACCAA CCATTCAATG GTTTAAGGAC      120
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TTCTTTCTCA AGGTTATCCA CTCACGTAGA GAGAGCGATG CGGGCACTTA CTGGTGCGAG      240
GCCAAAAACG AGTTTGGAGT GGCACGGTCC AGGAATGCAA CGTTGCAAGT GGCAGTTCTC      300
CGCGACGAAT TCCGTTTGGA GCCGGCAAAT ACCCGCGTGG CCCAAGGCGA GGTGGCCCTG      360
ATGGAATGCG GTGCCCCCG AGGATCTCCG GAGCCGCAAA TCTCGTGGCG CAAGAACGGC      420
CAGACCCTGA ATCTTGTCGG GAACAAGCGG ATTCGCATTG TCGACGGTGG CAATCTGGCC      480
ATCCAGGAAG CCCGCCAATC GGACGACGGA CGCTACCAGT GTGTGGTCAA GAATGTGGTT      540
GGCACCCGGG AGTCGGCCAC CGCTTTTCTT AAAGTGCATG TACGTCCATT CCTCATCCGA      600
GGACCCCAGA ATCAGACGGC GGTGGTGGGC AGCTCGGTGG TCTTCCAGTG CCGCATCGGA      660
GGCGATCCCC TGCCTGATGT CCTGTGGCGA CGCACTGCCT CCGGCGGCAA TATGCCACTG      720
CGTAAGTTTT CTTGGCTTCA TTCAGCTTCA GGTCGTGTGC ACGTACTTGA GGACCGCAGT      780
CTGAAGCTGG ACGACGTTAC TCTGGAGGAC ATGGGCGAGT ACACTTGCGA GGCGGACAAT      840
GCGGTGGGCG GCATCACGGC CACTGGCATC CTCACCGTTC ACGCTCCCCC CAAATTTGTG      900
ATACGCCCCA AGAATCAGCT GGTGGAGATC GGTGATGAAG TGCTGTTCGA GTGCCAAGCG      960
AATGGACATC CCCGACCAAC GCTCTACTGG TCGGTGGAGG GCAACAGCTC CCTGCTGCTC     1020
CCCGGCTATC GGGATGGCCG CATGGAAGTG ACCCTGACGC CCGAGGGGCG CTCGGTGCTC     1080
TCGATAGCTC GATTTGCCCG TGAGGATTCC GGAAAGGTGG TCACTTGCAA CGCCCTGAAC     1140
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AGTCTGGTGG GCTATGTAAT CGAGATGTTT GGCAAAAACG AAACGGATGG CTGGGTGGCT     1680
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GAACCCATTA CGGTGGGAAC GCGCTACTTC AATAGTGGTC TGGATCTGAG CGAGGCTCGT     1860
GCCAGTCTGC TGTCCGGAGA TGTTGTGGAG CTGAGCAACG CCAGTGTGGT GGACTCCACT     1920
AGCATGAAAC TCACCTGGCA GATCATCAAT GGCAAATACG TCGAGGGCTT CTATGTCTAT     1980
GCGAGACAGT TGCCAAATCC AATAGTCAAC AATCCGGCGC CGTTACTAG CAATACCAAT     2040
CCGCTGCTGG GCTCTACATC CACATCCGCA TCCGCATCCG CCTCGGCATC GGCATTGATT     2100
TCGACAAAGC CAAATATTGC AGCTGCCGGC AAACGTGATG GGGAGACAAA CCAGAGTGGA     2160
GGAGGAGCTC CGACCCCACT GAACACCAAG TATCGCATGC TAACGATTCT CAATGGCGGT     2220
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GGCGCCTCAT CCTGCACCAT CACCGGGCTC GTCCAGTACA CGCTGTATGA ATTTTTCATC       2280
GTGCCATTTT ACAAATCCGT CGAGGGCAAG CCGTCGAATT CGCGCATCGC TCGCACCCTT       2340
GAAGATGTTC CCTCTGAGGC ACCATATGGA ATGGAGGCTC TGCTGTTGAA CTCCTCCGCG       2400
GTCTTCCTCA AATGGAAGGC ACCAGAACTC AAGGATCGGC ATGGTGTTCT CTTGAACTAT       2460
CATGTTATAG TCCGAGGTAT TGACACTGCC CACAATTTCT CACGCATTTT GACAAATGTC       2520
ACCATCGATG CCGCTTCGCC TACTCTGGTT TTGGCCAATC TCACCGAAGG CGTCATGTAC       2580
ACCGTGGGCG TGGCGGCCGG AAATAACGCT GGAGTTGGTC CTTATTGTGT CCCAGCTACT       2640
TTGCGTTTGG ATCCCATCAC AAAGCGACTC GATCCGTTCA TCAATCAGCG GGACCATGTT       2700
AACGATGTGC TGACGCAGCC CTGGTTCATA ATACTCCTGG GCGCCATCCT GGCCGTTCTT       2760
ATGCTGTCCT TTGGCGCAAT GGTCTTTGTG AAGCGCAAGC ACATGATGAT GAAGCAGTCG       2820
GCCCTAAATA CAATGCGTGG CAATCACACG AGCGACGTGC TCAAAATGCC GAGTCTATCG       2880
GCGCGCAATG GAAACGGCTA CTGGCTGGAC TCCTCCACCG GCGGAATGGT GTGGCGTCCC       2940
TCGCCCGGCG GCGACTCGCT GGAGATGCAA AAGGATCACA TCGCCGACTA TGCGCCGGTC       3000
TGCGGTGCCC CCGGTTCTCC GGCCGGCGGT GGCACCTCTT CCGGTGGATC CGGTGGCGCG       3060
GGCAGCGGTG CCAGCGGCGG CGATGACATT CATGGAGGAC ACGGCAGCGA ACGCAATCAG       3120
CAGCGGTACG TGGGCGAGTA CTCCAACATA CCGACCGACT ATGCAGAGGT GTCCAGTTTT       3180
GGCAAGGCAC CCAGCGAGTA TGGTCGGCAT GGCAACGCCT CCCCGGCCCC TTATGCCACC       3240
TCTTCGATCC TGAGTCCCCA CCAGCAGCAA CAGCAGCAGC AGCCGCGTTA TCAACAGCGA       3300
CCAGTGCCCG GCTATGGGCT CCAGCGCCCA ATGCACCCAC ACTACCAGCA GCAGCAGCAT       3360
CAGCAGCAAC AGGCGCAGCA GACGCACCAG CAACACCAGG CTCTCCAGCA GCACCAGCAA       3420
CTGCCACCCA GCAACATCTA CCAGCAGATG TCCACCACCA GCGAGATATA CCCCACGAAC       3480
ACGGGTCCTT CGCGCTCTGT CTACTCTGAG CAGTATTACT ACCCCAAGGA CAAGCAGAGA       3540
CACATCCACA TCACCGAGAA CAAGCTGAGC AACTGCCACA CCTATGAGGC GGCTCCTGGC       3600
GCCAAGCAGT CCTCGCCGAT ATCCTCGCAG TTCGCCAGCG TGAGGCGGCA GCAGCTGCCG       3660
CCCAACTGCA GCATCGGCAG GGAAAGTGCC CGCTTCAAGG TGCTAAACAC GGATCAGGGC       3720
AAGAACCAGC AGAATCTCCT GGATCTCGAC GGCTCCTCGA TGTGCTACAA CGGTCTGGCA       3780
GACTCGGGCT GCGGTGGATC TCCCTCCCCG ATGGCCATGC TGATGTCGCA CGAGGACGAG       3840
CACGCGCTGT ACCACACGGC GGATGGGGAT CTGGACGACA TGGAACGACT GTACGTCAAG       3900
GTGGACGAGC AGCAGCCTCC ACAGCAGCAG CAGCAGCTGA TTCCCCTGGT CCCACAGCAT       3960
CCGGCGGAAG GTCACCTGCA GTCCTGGCGG AATCAGAGCA CGCGGAGCAG TCGGAAGAAC       4020
GGCCAGGAAT GCATCAAGGA ACCCAGCGAG TTGATCTACG CTCCGGGAAG CGTGGCCAGC       4080
GAACGGAGCC TCCTCAGCAA CTCGGGTAGC GGCACCAGCA GCCAGCCAGC TGGCCACAAT       4140
GTCTGA                                                                  4146
```

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 1381 amino acids

        (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Gly Glu Asn Pro Arg Ile Ile Glu His Pro Met Asp Thr Thr Val Pro
1               5                   10                  15
Lys Asn Asp Pro Phe Thr Phe Asn Cys Gln Ala Glu Gly Asn Pro Thr
                20                  25                  30
Pro Thr Ile Gln Trp Phe Lys Asp Gly Arg Glu Leu Lys Thr Asp Thr
            35                  40                  45
Gly Ser His Arg Ile Met Leu Pro Ala Gly Gly Leu Phe Phe Leu Lys
    50                  55                  60
Val Ile His Ser Arg Arg Glu Ser Asp Ala Gly Thr Tyr Trp Cys Glu
65                  70                  75                  80
Ala Lys Asn Glu Phe Gly Val Ala Arg Ser Arg Asn Ala Thr Leu Gln
                85                  90                  95
Val Ala Val Leu Arg Asp Glu Phe Arg Leu Glu Pro Ala Asn Thr Arg
                100                 105                 110
Val Ala Gln Gly Glu Val Ala Leu Met Glu Cys Gly Ala Pro Arg Gly
                115                 120                 125
Ser Pro Glu Pro Gln Ile Ser Trp Arg Lys Asn Gly Gln Thr Leu Asn
    130                 135                 140
Leu Val Gly Asn Lys Arg Ile Arg Ile Val Asp Gly Gly Asn Leu Ala
145                 150                 155                 160
Ile Gln Glu Ala Arg Gln Ser Asp Asp Gly Arg Tyr Gln Cys Val Val
                165                 170                 175
Lys Asn Val Val Gly Thr Arg Glu Ser Ala Thr Ala Phe Leu Lys Val
                180                 185                 190
His Val Arg Pro Phe Leu Ile Arg Gly Pro Gln Asn Gln Thr Ala Val
            195                 200                 205
Val Gly Ser Ser Val Val Phe Gln Cys Arg Ile Gly Gly Asp Pro Leu
    210                 215                 220
Pro Asp Val Leu Trp Arg Arg Thr Ala Ser Gly Gly Asn Met Pro Leu
225                 230                 235                 240
Arg Lys Phe Ser Trp Leu His Ser Ala Ser Gly Arg Val His Val Leu
                245                 250                 255
Glu Asp Arg Ser Leu Lys Leu Asp Asp Val Thr Leu Glu Asp Met Gly
            260                 265                 270
```

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Glu Tyr Thr Cys Glu Ala Asp Asn Ala Val Gly Gly Ile Thr Ala Thr
        275   280   285

Gly Ile Leu Thr Val His Ala Pro Pro Lys Phe Val Ile Arg Pro Lys
        290   295   300

Asn Gln Leu Val Glu Ile Gly Asp Glu Val Leu Phe Glu Cys Gln Ala
305   310   315   320

Asn Gly His Pro Arg Pro Thr Leu Tyr Trp Ser Val Glu Gly Asn Ser
                325   330   335

Ser Leu Leu Leu Pro Gly Tyr Arg Asp Gly Arg Met Glu Val Thr Leu
                340   345   350

Thr Pro Glu Gly Arg Ser Val Leu Ser Ile Ala Arg Phe Ala Arg Glu
        355   360   365

Asp Ser Gly Lys Val Val Thr Cys Asn Ala Leu Asn Ala Val Gly Ser
        370   375   380

Val Ser Ser Arg Thr Val Val Ser Val Asp Thr Gln Phe Glu Leu Pro
385   390   395   400

Pro Pro Ile Ile Glu Gln Gly Pro Val Asn Gln Thr Leu Pro Val Lys
                405   410   415

Ser Ile Val Val Leu Pro Cys Arg Thr Leu Gly Thr Pro Val Pro Gln
                420   425   430

Val Ser Trp Tyr Leu Asp Gly Ile Pro Ile Asp Val Gln Glu His Glu
        435   440   445

Arg Arg Asn Leu Ser Asp Ala Gly Ala Leu Thr Ile Ser Asp Leu Gln
        450   455   460

Arg His Glu Asp Glu Gly Leu Tyr Thr Cys Val Ala Ser Asn Arg Asn
465   470   475   480

Gly Lys Ser Ser Trp Ser Gly Tyr Leu Arg Leu Asp Thr Pro Thr Asn
                485   490   495

Pro Asn Ile Lys Phe Phe Arg Ala Pro Glu Leu Ser Thr Tyr Pro Gly
                500   505   510

Pro Pro Gly Lys Pro Gln Met Val Glu Lys Gly Glu Asn Ser Val Thr
        515   520   525

Leu Ser Trp Thr Arg Ser Asn Lys Val Gly Gly Ser Ser Leu Val Gly
        530   535   540

Tyr Val Ile Glu Met Phe Gly Lys Asn Glu Thr Asp Gly Trp Val Ala
545   550   555   560

Val Gly Thr Arg Val Gln Asn Thr Thr Phe Thr Gln Thr Gly Leu Leu
                565   570   575

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```
Pro Gly Val Asn Tyr Phe Phe Leu Ile Arg Ala Glu Asn Ser His Gly
            580                 585                 590

Leu Ser Leu Pro Ser Pro Met Ser Glu Pro Ile Thr Val Gly Thr Arg
            595                 600                 605

Tyr Phe Asn Ser Gly Leu Asp Leu Ser Glu Ala Arg Ala Ser Leu Leu
    610                 615                 620

Ser Gly Asp Val Val Glu Leu Ser Asn Ala Ser Val Val Asp Ser Thr
625                 630                 635                 640

Ser Met Lys Leu Thr Trp Gln Ile Ile Asn Gly Lys Tyr Val Glu Gly
            645                 650                 655

Phe Tyr Val Tyr Ala Arg Gln Leu Pro Asn Pro Ile Val Asn Asn Pro
            660                 665                 670

Ala Pro Val Thr Ser Asn Thr Asn Pro Leu Leu Gly Ser Thr Ser Thr
            675                 680                 685

Ser Ala Ser Ala Ser Ala Ser Ala Ser Ala Leu Ile Ser Thr Lys Pro
            690                 695                 700

Asn Ile Ala Ala Ala Gly Lys Arg Asp Gly Glu Thr Asn Gln Ser Gly
705                 710                 715                 720

Gly Gly Ala Pro Thr Pro Leu Asn Thr Lys Tyr Arg Met Leu Thr Ile
            725                 730                 735

Leu Asn Gly Gly Gly Ala Ser Ser Cys Thr Ile Thr Gly Leu Val Gln
            740                 745                 750

Tyr Thr Leu Tyr Glu Phe Phe Ile Val Pro Phe Tyr Lys Ser Val Glu
            755                 760                 765

Gly Lys Pro Ser Asn Ser Arg Ile Ala Arg Thr Leu Glu Asp Val Pro
    770                 775                 780

Ser Glu Ala Pro Tyr Gly Met Glu Ala Leu Leu Leu Asn Ser Ser Ala
785                 790                 795                 800

Val Phe Leu Lys Trp Lys Ala Pro Glu Leu Lys Asp Arg His Gly Val
            805                 810                 815

Leu Leu Asn Tyr His Val Ile Val Arg Gly Ile Asp Thr Ala His Asn
            820                 825                 830

Phe Ser Arg Ile Leu Thr Asn Val Thr Ile Asp Ala Ala Ser Pro Thr
            835                 840                 845

Leu Val Leu Ala Asn Leu Thr Glu Gly Val Met Tyr Thr Val Gly Val
    850                 855                 860

Ala Ala Gly Asn Asn Ala Gly Val Gly Pro Tyr Cys Val Pro Ala Thr
865                 870                 875                 880
```

Leu Arg Leu Asp Pro Ile Thr Lys Arg Leu Asp Pro Phe Ile Asn Gln
                885   890   895

Arg Asp His Val Asn Asp Val Leu Thr Gln Pro Trp Phe Ile Ile Leu
            900   905   910

Leu Gly Ala Ile Leu Ala Val Leu Met Leu Ser Phe Gly Ala Met Val
            915   920   925

Phe Val Lys Arg Lys His Met Met Met Lys Gln Ser Ala Leu Asn Thr
        930   935   940

Met Arg Gly Asn His Thr Ser Asp Val Leu Lys Met Pro Ser Leu Ser
945   950   955   960

Ala Arg Asn Gly Asn Gly Tyr Trp Leu Asp Ser Ser Thr Gly Gly Met
                965   970   975

Val Trp Arg Pro Ser Pro Gly Gly Asp Ser Leu Glu Met Gln Lys Asp
            980   985   990

His Ile Ala Asp Tyr Ala Pro Val Cys Gly Ala Pro Gly Ser Pro Ala
            995   1000   1005

Gly Gly Gly Thr Ser Ser Gly Gly Ser Gly Gly Ala Gly Ser Gly Ala
        1010   1015   1020

Ser Gly Gly Asp Asp Ile His Gly Gly His Gly Ser Glu Arg Asn Gln
1025   1030   1035   1040

Gln Arg Tyr Val Gly Glu Tyr Ser Asn Ile Pro Thr Asp Tyr Ala Glu
            1045   1050   1055

Val Ser Ser Phe Gly Lys Ala Pro Ser Glu Tyr Gly Arg His Gly Asn
            1060   1065   1070

Ala Ser Pro Ala Pro Tyr Ala Thr Ser Ser Ile Leu Ser Pro His Gln
            1075   1080   1085

Gln Gln Gln Gln Gln Gln Pro Arg Tyr Gln Gln Arg Pro Val Pro Gly
        1090   1095   1100

Tyr Gly Leu Gln Arg Pro Met His Pro His Tyr Gln Gln Gln Gln His
1105   1110   1115   1120

Gln Gln Gln Gln Ala Gln Gln Thr His Gln Gln His Gln Ala Leu Gln
                1125   1130   1135

Gln His Gln Gln Leu Pro Pro Ser Asn Ile Tyr Gln Gln Met Ser Thr
            1140   1145   1150

Thr Ser Glu Ile Tyr Pro Thr Asn Thr Gly Pro Ser Arg Ser Val Tyr
            1155   1160   1165

Ser Glu Gln Tyr Tyr Tyr Pro Lys Asp Lys Gln Arg His Ile His Ile
            1170   1175   1180

```
Thr Glu Asn Lys Leu Ser Asn Cys His Thr Tyr Glu Ala Ala Pro Gly
1185                1190            1195                1200
Ala Lys Gln Ser Ser Pro Ile Ser Ser Gln Phe Ala Ser Val Arg Arg
              1205            1210                1215
Gln Gln Leu Pro Pro Asn Cys Ser Ile Gly Arg Glu Ser Ala Arg Phe
              1220            1225            1230
Lys Val Leu Asn Thr Asp Gln Gly Lys Asn Gln Gln Asn Leu Leu Asp
              1235            1240            1245
Leu Asp Gly Ser Ser Met Cys Tyr Asn Gly Leu Ala Asp Ser Gly Cys
          1250            1255                1260
Gly Gly Ser Pro Ser Pro Met Ala Met Leu Met Ser His Glu Asp Glu
1265                1270            1275                1280
His Ala Leu Tyr His Thr Ala Asp Gly Asp Leu Asp Asp Met Glu Arg
              1285            1290            1295
Leu Tyr Val Lys Val Asp Glu Gln Gln Pro Pro Gln Gln Gln Gln Gln
              1300            1305            1310
Leu Ile Pro Leu Val Pro Gln His Pro Ala Glu Gly His Leu Gln Ser
          1315            1320            1325
Trp Arg Asn Gln Ser Thr Arg Ser Ser Arg Lys Asn Gly Gln Glu Cys
          1330            1335            1340
Ile Lys Glu Pro Ser Glu Leu Ile Tyr Ala Pro Gly Ser Val Ala Ser
1345                1350            1355                1360
Glu Arg Ser Leu Leu Ser Asn Ser Gly Ser Gly Thr Ser Ser Gln Pro
              1365            1370            1375
Ala Gly His Asn Val
          1380
```

(2) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 3894 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: double

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
ATGTACTATC TAGGTTTTTA CCACACTCAC ACACACACAC ACACATACAT AAATTTTGAT     60
AAAATTCCTA ATGCCTCAAA TCTCGCTCCC GTGATAATCG AACATCCCAT CGATGTGGTG    120
GTATCTAGGG GATCGCCAGC AACCCTCAAC TGTGGTGCAA AGCCATCTAC CGCCAAAATC    180
```

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ACATGGTACA AGGATGGACA GCCCGTAATC ACGAATAAGG AGCAAGTGAA CAGCCACCGG      240

ATTGTTCTCG ACACGGGATC CCTGTTTCTT CTGAAAGTGA ATAGTGGAAA AAACGGAAAA      300

GACAGCGATG CGGGAGCGTA CTATTGTGTG GCCAGCAACG AGCACGGAGA AGTGAAGTCG      360

AACGAAGGAT CGTTAAAATT GGCGATGCTT CGCGAAGACT TTCGAGTTCG GCCAAGAACA      420

GTTCAGGCTC TTGGTGGAGA GATGGCCGTT CTGGAATGCA GTCCGCCACG TGGATTCCCG      480

GAGCCGGTTG TGAGCTGGCG GAAAGACGAC AAAGAGCTCC GAATTCAAGA CATGCCACGA      540

TACACTCTAC ACTCTGACGG AAACCTCATC ATTGATCCGG TCGATCGAAG CGATTCTGGT      600

ACTTATCAGT GTGTTGCCAA CAACATGGTC GGAGAACGGG TGTCCAATCC CGCAAGATTG      660

AGTGTCTTTG AGAAACCAAA GTTTGAGCAA GAACCCAAGG ACATGACGGT CGACGTCGGA      720

GCCGCAGTGC TGTTTGATTG TCGTGTGACT GGAGATCCTC AACCACAAAT TACGTGGAAA      780

CGCAAAAATG AGCCGATGCC AGTTACACGT GCATACATTG CCAAGGATAA TCGGGGGTTG      840

AGAATCGAAA GAGTTCAACC ATCAGACGAA GGTGAATACG TTTGCTATGC ACGAAATCCA      900

GCGGGAACTC TTGAAGCATC TGCACATCTT CGTGTCCAGG CACCTCCATC CTTCCAGACA      960

AAACCAGCAG ACCAGTCAGT TCCAGCTGGA GGCACGGCAA CTTTTGAATG CACCTTGGTC     1020

GGTCAACCGA GTCCCGCCTA TTTTTGGAGC AAGGAAGGCC AACAGGATCT TCTTTTCCCA     1080

AGTTATGTGT CCGCTGATGG TAGAACGAAA GTTTCACCAA CTGGAACATT GACAATTGAG     1140

GAAGTTCGTC AAGTTGATGA GGGAGCTTAT GTGTGCGCTG GAATGAACTC GGCAGGAAGC     1200

TCGTTGAGCA AGGCAGCTTT GAAAGCAACA TTTGAAACCA AAGGCCGTGT CCAAAAAAAA     1260

AAGAGCAAAA TGGGCAAACA GAAACAAAAA AATGTTCAAT CAATTATCAA ATATTTAATT     1320

TCAGCCGTGA CCGGAAACAC ACCCGCCAAA CCACCACCAA CAATCGAGCA TGGTCATCAA     1380

AATCAGACCC TTATGGTTGG ATCATCAGCC ATCCTTCCAT GTCAGGCTAG CGGAAAACCA     1440

ACTCCAGGAA TATCATGGCT CAGGGATGGG CTACCTATTG ACATTACAGA TAGTCGTATC     1500

AGTCAACATT CAACGGGAAG TCTACATATT GCCGATTTAA AGAAACCTGA CACCGGAGTT     1560

TACACTTGCA TTGCGAAGAA CGAGGATGGA GAGTCAACAT GGTCGGCATC TCTGACTGTT     1620

GAAGATCACA CTAGCAATGC ACAATTTGTT CGGATGCCGG ATCCATCGAA CTTCCCGTCT     1680

TCTCCAACGC AACCCATTAT TGTCAATGTC ACTGATACCG AAGTAGAGCT CCACTGGAAT     1740

GCTCCCTCCA CATCTGGCGC AGGACCAATC ACTGGTTATA TCATTCAGTA CTACAGTCCA     1800

GACCTCGGAC AGACGTGGTT TAACATTCCA GACTACGTGG CATCTACTGA ATATAGAATA     1860

AAGGGTCTGA AACCATCTCA CTCGTATATG TTTGTGATTC GAGCAGAAAA TGAGAAAGGT     1920

ATTGGAACGC CGAGTGTGTC GTCGGCTCTC GTTACCACTA GCAAGCCAGC AGCTCAAGTT     1980

GCGCTTTCTG ACAAGAACAA AATGGACATG GCCATCGCTG AGAAGAGACT CACTTCGGAA     2040

CAACTCATAA AACTCGAGGA AGTGAAGACT ATTAATTCTA CGGCCGTTCG TTTGTTCTGG     2100

AAGAAGAGGA AACTTGAAGA GCTGATTGAT GGTTACTACA TCAAGTGGAG AGGGCCTCCA     2160

AGAACCAATG ATAATCAATA CGTGAATGTG ACCAGCCCTA GCACCGAAAA CTATGTTGTT     2220

TCAAATTTAA TGCCATTCAC CAACTATGAG TTTTTCGTGA TTCCTTATCA TTCCGGAGTT     2280

CATAGTATTC ATGGAGCACC GAGTAATTCC ATGGACGTGT TGACCGCCGA AGCTCCACCT     2340

TCATTGCCAC CAGAGGATGT GCGAATCCGT ATGCTCAACC TGACCACTCT TCGTATCTCT     2400

TGGAAAGCAC CAAAAGCCGA CGGCATCAAC GGAATTCTCA AAGGATTCCA AATTGTTATT     2460
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GTTGGTCAAG CGCCCAACAA CAATCGGAAC ATCACTACAA ACGAGAGAGC TGCCAGTGTT      2520

ACTCTGTTCC ATTTAGTGAC TGGAATGACG TATAAAATTC GTGTAGCGGC TAGAAGCAAT      2580

GGTGGAGTTG GAGTCTCACA TGGAACGAGT GAAGTCATCA TGAATCAAGA CACGCTGGAA      2640

AAACACCTTG CTGCTCAACA AGAAAACGAA TCATTTTTGT ATGGGCTGAT CAATAAATCT      2700

CATGTTCCTG TGATTGTCAT TGTTGCAATT CTGATTATTT TCGTAGTCAT CATTATAGCC      2760

TATTGTTACT GGAGGAATAG CAGAAACAGT GATGGAAAGG ATCGAAGTTT TATAAAGATC      2820

AATGATGGAA GTGTTCATAT GGCTTCGAAT AATCTTTGGG ATGTTGCACA AAATCCGAAT      2880

CAGAATCCAA TGTACAACAC TGCTGGAAGA ATGACTATGA ACAATAGAAA TGGCCAGGCT      2940

CTCTATTCGC TGACACCAAA TGCGCAAGAC TTTTTCAACA ATTGTGATGA CTACAGTGGA      3000

ACGATGCACA GACCAGGATC CGAGCATCAC TATCATTATG CTCAACTGAC TGGCGGACCT      3060

GGTAATGCGA TGTCTACTTT TTATGGAAAC CAATATCACG ATGATCCATC TCCATATGCC      3120

ACCACAACAC TGGTCCTGTC GAACCAACAA CCAGCTTGGC TCAATGACAA AATGCTTCGC      3180

GCGCCAGCAA TGCCAACAAA TCCCGTGCCA CCAGAGCCAC CGGCGCGATA TGCAGATCAT      3240

ACCGCTGGAA GACGATCTCG ATCGAGCCGT GCATCCGATG GGAGAGGAAC TCTGAATGGC      3300

GGACTCCATC ACCGGACTAG CGGAAGTCAA CGGTCGGATA GTCCACCTCA CACAGATGTG      3360

AGCTATGTTC AGCTTCACTC ATCCGATGGA ACTGGTAGTA GTAAGGAAAG AACTGGGGAG      3420

CGGAGAACAC CACCGAATAA GACTCTGATG GACTTTATTC CGCCACCACC TTCCAATCCA      3480

CCACCACCTG GAGGGCACGT TTATGACACA GCAACTAGGC GTCAGTTGAA TCGTGGAAGT      3540

ACTCCACGAG AAGACACCTA CGATTCGGTC AGTGACGGAG CTTTTGCTCG GGTTGATGTG      3600

AATGCAAGGC CAACGAGTCG GAATCGGAAT TTGGGAGGAA GGCCGCTGAA AGGGAAACGA      3660

GACGACGATA GTCAGCGGTC TTCGTTGATG ATGGACGATG ATGGTGGATC TTCTGAAGCT      3720

GACGGGGAGA ACTCTGAAGG AGACGTTCCG CGTGGAGGTG TTAGAAAAGC AGTTCCTCGA      3780

ATGGGTATCT CTGCAAGTAC GCTGGCTCAT AGTTGTTACG GGACAAACGG CACTGCTCAA      3840

CGATTCCGGT CAATTCCACG TAACAATGGA ATCGTCACAC AAGAACAAAC TTGA          3894
```

(2) INFORMATION FOR SEQ ID NO:6:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 1297 amino acids

        (B) TYPE: amino acid

        (C) STRANDEDNESS: single

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Met Tyr Tyr Leu Gly Phe Tyr His Thr His Thr His Thr His Thr Tyr
1               5                   10                  15

Ile Asn Phe Asp Lys Ile Pro Asn Ala Ser Asn Leu Ala Pro Val Ile
                20                  25                  30

Ile Glu His Pro Ile Asp Val Val Val Ser Arg Gly Ser Pro Ala Thr
```

Leu Asn Cys Gly Ala Lys Pro Ser Thr Ala Lys Ile Thr Trp Tyr Lys

    50   55   60

Asp Gly Gln Pro Val Ile Thr Asn Lys Glu Gln Val Asn Ser His Arg

65   70   75   80

Ile Val Leu Asp Thr Gly Ser Leu Phe Leu Leu Lys Val Asn Ser Gly

              85   90   95

Lys Asn Gly Lys Asp Ser Asp Ala Gly Ala Tyr Tyr Cys Val Ala Ser

            100   105   110

Asn Glu His Gly Glu Val Lys Ser Asn Glu Gly Ser Leu Lys Leu Ala

            115   120   125

Met Leu Arg Glu Asp Phe Arg Val Arg Pro Arg Thr Val Gln Ala Leu

    130   135   140

Gly Gly Glu Met Ala Val Leu Glu Cys Ser Pro Pro Arg Gly Phe Pro

145   150   155   160

Glu Pro Val Val Ser Trp Arg Lys Asp Asp Lys Glu Leu Arg Ile Gln

            165   170   175

Asp Met Pro Arg Tyr Thr Leu His Ser Asp Gly Asn Leu Ile Ile Asp

            180   185   190

Pro Val Asp Arg Ser Asp Ser Gly Thr Tyr Gln Cys Val Ala Asn Asn

            195   200   205

Met Val Gly Glu Arg Val Ser Asn Pro Ala Arg Leu Ser Val Phe Glu

    210   215   220

Lys Pro Lys Phe Glu Gln Glu Pro Lys Asp Met Thr Val Asp Val Gly

225   230   235   240

Ala Ala Val Leu Phe Asp Cys Arg Val Thr Gly Asp Pro Gln Pro Gln

            245   250   255

Ile Thr Trp Lys Arg Lys Asn Glu Pro Met Pro Val Thr Arg Ala Tyr

            260   265   270

Ile Ala Lys Asp Asn Arg Gly Leu Arg Ile Glu Arg Val Gln Pro Ser

            275   280   285

Asp Glu Gly Glu Tyr Val Cys Tyr Ala Arg Asn Pro Ala Gly Thr Leu

            290   295   300

Glu Ala Ser Ala His Leu Arg Val Gln Ala Pro Pro Ser Phe Gln Thr

305   310   315   320

Lys Pro Ala Asp Gln Ser Val Pro Ala Gly Gly Thr Ala Thr Phe Glu

            325   330   335

Cys Thr Leu Val Gly Gln Pro Ser Pro Ala Tyr Phe Trp Ser Lys Glu

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Gly Gln Gln Asp Leu Leu Phe Pro Ser Tyr Val Ser Ala Asp Gly Arg
          355   360   365
Thr Lys Val Ser Pro Thr Gly Thr Leu Thr Ile Glu Glu Val Arg Gln
        370   375   380
Val Asp Glu Gly Ala Tyr Val Cys Ala Gly Met Asn Ser Ala Gly Ser
385   390   395   400
Ser Leu Ser Lys Ala Ala Leu Lys Ala Thr Phe Glu Thr Lys Gly Arg
                  405   410   415
Val Gln Lys Lys Lys Ser Lys Met Gly Lys Gln Lys Gln Lys Asn Val
                  420   425   430
Gln Ser Ile Ile Lys Tyr Leu Ile Ser Ala Val Thr Gly Asn Thr Pro
          435   440   445
Ala Lys Pro Pro Pro Thr Ile Glu His Gly His Gln Asn Gln Thr Leu
        450   455   460
Met Val Gly Ser Ser Ala Ile Leu Pro Cys Gln Ala Ser Gly Lys Pro
465   470   475   480
Thr Pro Gly Ile Ser Trp Leu Arg Asp Gly Leu Pro Ile Asp Ile Thr
                  485   490   495
Asp Ser Arg Ile Ser Gln His Ser Thr Gly Ser Leu His Ile Ala Asp
                  500   505   510
Leu Lys Lys Pro Asp Thr Gly Val Tyr Thr Cys Ile Ala Lys Asn Glu
                  515   520   525
Asp Gly Glu Ser Thr Trp Ser Ala Ser Leu Thr Val Glu Asp His Thr
          530   535   540
Ser Asn Ala Gln Phe Val Arg Met Pro Asp Pro Ser Asn Phe Pro Ser
545   550   555   560
Ser Pro Thr Gln Pro Ile Ile Val Asn Val Thr Asp Thr Glu Val Glu
                  565   570   575
Leu His Trp Asn Ala Pro Ser Thr Ser Gly Ala Gly Pro Ile Thr Gly
                  580   585   590
Tyr Ile Ile Gln Tyr Tyr Ser Pro Asp Leu Gly Gln Thr Trp Phe Asn
                  595   600   605
Ile Pro Asp Tyr Val Ala Ser Thr Glu Tyr Arg Ile Lys Gly Leu Lys
          610   615   620
Pro Ser His Ser Tyr Met Phe Val Ile Arg Ala Glu Asn Glu Lys Gly
625   630   635   640
Ile Gly Thr Pro Ser Val Ser Ser Ala Leu Val Thr Thr Ser Lys Pro

Ala Ala Gln Val Ala Leu Ser Asp Lys Asn Lys Met Asp Met Ala Ile
            660   665   670
Ala Glu Lys Arg Leu Thr Ser Glu Gln Leu Ile Lys Leu Glu Glu Val
            675   680   685
Lys Thr Ile Asn Ser Thr Ala Val Arg Leu Phe Trp Lys Lys Arg Lys
            690   695   700
Leu Glu Glu Leu Ile Asp Gly Tyr Tyr Ile Lys Trp Arg Gly Pro Pro
705   710   715   720
Arg Thr Asn Asp Asn Gln Tyr Val Asn Val Thr Ser Pro Ser Thr Glu
                    725   730   735
Asn Tyr Val Val Ser Asn Leu Met Pro Phe Thr Asn Tyr Glu Phe Phe
                    740   745   750
Val Ile Pro Tyr His Ser Gly Val His Ser Ile His Gly Ala Pro Ser
                    755   760   765
Asn Ser Met Asp Val Leu Thr Ala Glu Ala Pro Pro Ser Leu Pro Pro
            770   775   780
Glu Asp Val Arg Ile Arg Met Leu Asn Leu Thr Thr Leu Arg Ile Ser
785   790   795   800
Trp Lys Ala Pro Lys Ala Asp Gly Ile Asn Gly Ile Leu Lys Gly Phe
                    805   810   815
Gln Ile Val Ile Val Gly Gln Ala Pro Asn Asn Asn Arg Asn Ile Thr
                    820   825   830
Thr Asn Glu Arg Ala Ala Ser Val Thr Leu Phe His Leu Val Thr Gly
            835   840   845
Met Thr Tyr Lys Ile Arg Val Ala Ala Arg Ser Asn Gly Gly Val Gly
            850   855   860
Val Ser His Gly Thr Ser Glu Val Ile Met Asn Gln Asp Thr Leu Glu
865   870   875   880
Lys His Leu Ala Ala Gln Gln Glu Asn Glu Ser Phe Leu Tyr Gly Leu
                    885   890   895
Ile Asn Lys Ser His Val Pro Val Ile Val Ile Val Ala Ile Leu Ile
                    900   905   910
Ile Phe Val Val Ile Ile Ile Ala Tyr Cys Tyr Trp Arg Asn Ser Arg
                    915   920   925
Asn Ser Asp Gly Lys Asp Arg Ser Phe Ile Lys Ile Asn Asp Gly Ser
            930   935   940
Val His Met Ala Ser Asn Asn Leu Trp Asp Val Ala Gln Asn Pro Asn

Gln Asn Pro Met Tyr Asn Thr Ala Gly Arg Met Thr Met Asn Asn Arg
                965   970   975

Asn Gly Gln Ala Leu Tyr Ser Leu Thr Pro Asn Ala Gln Asp Phe Phe
          980   985   990

Asn Asn Cys Asp Asp Tyr Ser Gly Thr Met His Arg Pro Gly Ser Glu
        995   1000   1005

His His Tyr His Tyr Ala Gln Leu Thr Gly Gly Pro Gly Asn Ala Met
      1010   1015   1020

Ser Thr Phe Tyr Gly Asn Gln Tyr His Asp Asp Pro Ser Pro Tyr Ala
1025   1030   1035   1040

Thr Thr Thr Leu Val Leu Ser Asn Gln Gln Pro Ala Trp Leu Asn Asp
                1045   1050   1055

Lys Met Leu Arg Ala Pro Ala Met Pro Thr Asn Pro Val Pro Pro Glu
            1060   1065   1070

Pro Pro Ala Arg Tyr Ala Asp His Thr Ala Gly Arg Arg Ser Arg Ser
            1075   1080   1085

Ser Arg Ala Ser Asp Gly Arg Gly Thr Leu Asn Gly Gly Leu His His
          1090   1095   1100

Arg Thr Ser Gly Ser Gln Arg Ser Asp Ser Pro Pro His Thr Asp Val
1105   1110   1115   1120

Ser Tyr Val Gln Leu His Ser Ser Asp Gly Thr Gly Ser Ser Lys Glu
                1125   1130   1135

Arg Thr Gly Glu Arg Arg Thr Pro Pro Asn Lys Thr Leu Met Asp Phe
            1140   1145   1150

Ile Pro Pro Pro Pro Ser Asn Pro Pro Pro Gly Gly His Val Tyr
            1155   1160   1165

Asp Thr Ala Thr Arg Arg Gln Leu Asn Arg Gly Ser Thr Pro Arg Glu
      1170   1175   1180

Asp Thr Tyr Asp Ser Val Ser Asp Gly Ala Phe Ala Arg Val Asp Val
1185   1190   1195   1200

Asn Ala Arg Pro Thr Ser Arg Asn Arg Asn Leu Gly Gly Arg Pro Leu
                1205   1210   1215

Lys Gly Lys Arg Asp Asp Asp Ser Gln Arg Ser Ser Leu Met Met Asp
            1220   1225   1230

Asp Asp Gly Gly Ser Ser Glu Ala Asp Gly Glu Asn Ser Glu Gly Asp
          1235   1240   1245

Val Pro Arg Gly Gly Val Arg Lys Ala Val Pro Arg Met Gly Ile Ser

```
            1250                 1255                  1260
       Ala Ser Thr Leu Ala His Ser Cys Tyr Gly Thr Asn Gly Thr Ala Gln
            1265                 1270                  1275            1280
       Arg Phe Arg Ser Ile Pro Arg Asn Asn Gly Ile Val Thr Gln Glu Gln
                            1285                 1290            1295
       Thr
```

(2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 4956 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: double

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
ATGAAATGGA AACATGTTCC TTTTTTGGTC ATGATATCAC TCCTCAGCTT ATCCCCAAAT      60
CACCTGTTTC TGGCCCAGCT TATTCCAGAC CCTGAAGATG TAGAGAGGGG GAACGACCAC     120
GGGACGCCAA TCCCCACCTC TGATAACGAT GACAATTCGC TGGGCTATAC AGGCTCCCGT     180
CTTCGTCAGG AAGATTTTCC ACCTCGCATT GTTGAACACC CTTCAGACCT GATTGTCTCA     240
AAAGGAGAAC CTGCAACTTT GAACTGCAAA GCTGAAGGCC GCCCCACACC CACTATTGAA     300
TGGTACAAAG GGGGAGAGAG AGTGGAGACA GACAAAGATG ACCCTCGCTC ACACCGAATG     360
TTGCTGCCGA GTGGATCTTT ATTTTTCTTA CGTATAGTAC ATGGACGGAA AAGTAGACCT     420
GATGAAGGAG TCTATGTCTG TGTAGCAAGG AATTACCTTG AGAGGCTGT GAGCCACAAT     480
GCATCGCTGG AAGTAGCCAT ACTTCGGGAT GACTTCAGAC AAAACCCTTC GGATGTCATG     540
GTTGCAGTAG AGAGCCTGC AGTAATGGAA TGCCAACCTC CACGAGGCCA TCCTGAGCCC     600
ACCATTTCAT GGAAGAAAGA TGGCTCTCCA CTGGATGATA AGATGAAAG AATAACTATA     660
CGAGGAGGAA AGCTCATGAT CACTTACACC CGTAAAAGTG ACGCTGGCAA ATATGTTTGT     720
GTTGGTACCA ATATGGTTGG GGAACGTGAG AGTGAAGTAG CCGAGCTGAC TGTCTTAGAG     780
AGACCATCAT TTGTGAAGAG ACCCAGTAAC TTGGCAGTAA CTGTGGATGA CAGTGCAGAA     840
TTTAAATGTG AGGCCCGAGG TGACCCTGTA CCTACAGTAC GATGGAGGAA AGATGATGGA     900
GAGCTGCCCA AATCCAGATA TGAAATCCGA GATGATCATA CCTTGAAAAT TAGGAAGGTG     960
ACAGCTGGTG ACATGGGTTC ATACACTTGT GTTGCAGAAA ATATGGTGGG CAAAGCTGAA    1020
GCATCTGCTA CTCTGACTGT TCAAGAACCT CCACATTTTG TTGTGAAACC CCGTGACCAG    1080
GTTGTTGCTT TGGGACGGAC TGTAACTTTT CAGTGTGAAG CAACCGGAAA TCCTCAACCA    1140
GCTATTTTCT GGAGGAGAGA AGGGAGTCAG AATCTACTTT TCTCATATCA ACCACCACAG    1200
TCATCCAGCC GATTTTCAGT CTCCCAGACT GGCGACCTCA CAATTACTAA TGTCCAGCGA    1260
TCTGATGTTG GTTATTACAT CTGCCAGACT TTAAATGTTG CTGGAAGCAT CATCACAAAG    1320
GCATATTTGG AAGTTACAGA TGTGATTGCA GATCGGCCTC CCCCAGTTAT TCGACAAGGT    1380
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CCTGTGAATC AGACTGTAGC CGTGGATGGC ACTTTCGTCC TCAGCTGTGT GGCCACAGGC      1440

AGTCCAGTGC CCACCATTCT GTGGAGAAAG GATGGAGTCC TCGTTTCAAC CCAAGACTCT      1500

CGAATCAAAC AGTTGGAGAA TGGAGTACTG CAGATCCGAT ATGCTAAGCT GGGTGATACT      1560

GGTCGGTACA CCTGCATTGC ATCAACCCCC AGTGGTGAAG CAACATGGAG TGCTTACATT      1620

GAAGTTCAAG AATTTGGAGT TCCAGTTCAG CCTCCAAGAC CTACTGACCC AAATTTAATC      1680

CCTAGTGCCC CATCAAAACC TGAAGTGACA GATGTCAGCA GAAATACAGT CACATTATCG      1740

TGGCAACCAA ATTTGAATTC AGGAGCAACT CCAACATCTT ATATTATAGA AGCCTTCAGC      1800

CATGCATCTG GTAGCAGCTG GCAGACCGTA GCAGAGAATG TGAAAACAGA AACATCTGCC      1860

ATTAAAGGAC TCAAACCTAA TGCAATTTAC CTTTTCCTTG TGAGGGCAGC TAATGCATAT      1920

GGAATTAGTG ATCCAAGCCA AATATCAGAT CCAGTGAAAA CACAAGATGT CCTACCAACA      1980

AGTCAGGGGG TGGACCACAA GCAGGTCCAG AGAGAGCTGG GAAATGCTGT TCTGCACCTC      2040

CACAACCCCA CCGTCCTTTC TTCCTCTTCC ATCGAAGTGC ACTGGACAGT AGATCAACAG      2100

TCTCAGTATA TACAAGGATA TAAAATTCTC TATCGGCCAT CTGGAGCCAA CCACGGAGAA      2160

TCAGACTGGT TAGTTTTTGA AGTGAGGACG CCAGCCAAAA ACAGTGTGGT AATCCCTGAT      2220

CTCAGAAAGG GAGTCAACTA TGAAATTAAG GCTCGCCCTT TTTTTAATGA ATTTCAAGGA      2280

GCAGATAGTG AAATCAAGTT TGCCAAAACC CTGGAAGAAG CACCCAGTGC CCCACCCCAA      2340

GGTGTAACTG TATCCAAGAA TGATGGAAAC GGAACTGCAA TTCTAGTTAG TTGGCAGCCA      2400

CCTCCAGAAG ACACTCAAAA TGGAATGGTC CAAGAGTATA AGGTTTGGTG TCTGGGCAAT      2460

GAAACTCGAT ACCACATCAA CAAAACAGTG GATGGTTCCA CCTTTTCCGT GGTCATTCCC      2520

TTTCTTGTTC CTGGAATCCG ATACAGTGTG GAAGTGGCAG CCAGCACTGG GGCTGGGTCT      2580

GGGGTAAAGA GTGAGCCTCA GTTCATCCAG CTGGATGCCC ATGGAAACCC TGTGTCACCT      2640

GAGGACCAAG TCAGCCTCGC TCAGCAGATT TCAGATGTGG TGAAGCAGCC GGCCTTCATA      2700

GCAGGTATTG GAGCAGCCTG TTGGATCATC CTCATGGTCT TCAGCATCTG GCTTTATCGA      2760

CACCGCAAGA AGAGAAACGG ACTTACTAGT ACCTACGCGG GTATCAGAAA AGTCCCGTCT      2820

TTTACCTTCA CACCAACAGT AACTTACCAG AGAGGAGGCG AAGCTGTCAG CAGTGGAGGG      2880

AGGCCTGGAC TTCTCAACAT CAGTGAACCT GCCGCGCAGC CATGGCTGGC AGACACGTGG      2940

CCTAATACTG GCAACAACCA CAATGACTGC TCCATCAGCT GCTGCACGGC AGGCAATGGA      3000

AACAGCGACA GCAACCTCAC TACCTACAGT CGCCCAGCTG ATTGTATAGC AAATTATAAC      3060

AACCAACTGG ATAACAAACA AACAAATCTG ATGCTCCCTG AGTCAACTGT TTATGGTGAT      3120

GTGGACCTTA GTAACAAAAT CAATGAGATG AAAACCTTCA ATAGCCCAAA TCTGAAGGAT      3180

GGGCGTTTTG TCAATCCATC AGGGCAGCCT ACTCCTTACG CCACCACTCA GCTCATCCAG      3240

TCAAACCTCA GCAACAACAT GAACAATGGC AGCGGGGACT CTGGCGAGAA GCACTGGAAA      3300

CCACTGGGAC AGCAGAAACA AGAAGTGGCA CCAGTTCAGT ACAACATCGT GGAGCAAAAC      3360

AAGCTGAACA AAGATTATCG AGCAAATGAC ACAGTTCCTC AACTATCCCC ATACAACCAA      3420

TCATACGACC AGAACACAGG AGGATCCTAC AACAGCTCAG ACCGGGGCAG TAGTACATCT      3480

GGGAGTCAGG GGCACAAGAA AGGGGCAAGA ACACCCAAGG TACCAAAACA GGGTGGCATG      3540

AACTGGGCAG ACCTGCTTCC TCCTCCCCCA GCACATCCTC CTCCACACAG CAATAGCGAA      3600

GAGTACAACA TTTCTGTAGA TGAAAGCTAT GACCAAGAAA TGCCATGTCC CGTGCCACCA      3660
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GCAAGGATGT ATTTGCAACA AGATGAATTA GAAGAGGAGG AAGATGAACG AGGCCCCACT   3720

CCCCCTGTTC GGGGAGCAGC TTCTTCTCCA GCTGCCGTGT CCTATAGCCA TCAGTCCACT   3780

GCCACTCTGA CTCCCTCCCC ACAGGAAGAA CTCCAGCCCA TGTTACAGGA TTGTCCAGAG   3840

GAGACTGGCC ACATGCAGCA CCAGCCCGAC AGGAGACGGC AGCCTGTGAG TCCTCCTCCA   3900

CCACCACGGC CGATCTCCCC TCCACATACC TATGGCTACA TTTCAGGACC CCTGGTCTCA   3960

GATATGGATA CGGATGCGCC AGAAGAGGAA GAAGACGAAG CCGACATGGA GGTAGCCAAG   4020

ATGCAAACCA GAAGGCTTTT GTTACGTGGG CTTGAGCAGA CACCTGCCTC CAGTGTTGGG   4080

GACCTGGAGA GCTCTGTCAC GGGGTCCATG ATCAACGGCT GGGGCTCAGC CTCAGAGGAG   4140

GACAACATTT CCAGCGGACG CTCCAGTGTT AGTTCTTCGG ACGGCTCCTT TTTCACTGAT   4200

GCTGACTTTG CCCAGGCAGT CGCAGCAGCG GCAGAGTATG CTGGTCTGAA AGTAGCACGA   4260

CGGCAAATGC AGGATGCTGC TGGCCGTCGA CATTTTCATG CGTCTCAGTG CCCTAGGCCC   4320

ACAAGTCCCG TGTCTACAGA CAGCAACATG AGTGCCGCCG TAATGCAGAA AACCAGACCA   4380

GCCAAGAAAC TGAAACACCA GCCAGGACAT CTGCGCAGAG AAACCTACAC AGATGATCTT   4440

CCACCACCTC CTGTGCCGCC ACCTGCTATA AAGTCACCTA CTGCCCAATC CAAGACACAG   4500

CTGGAAGTAC GACCTGTAGT GGTGCCAAAA CTCCCTTCTA TGGATGCAAG AACAGACAGA   4560

TCATCAGACA GAAAAGGAAG CAGTTACAAG GGGAGAGAAG TGTTGGATGG AAGACAGGTT   4620

GTTGACATGC GAACAAATCC AGGTGATCCC AGAGAAGCAC AGGAACAGCA AAATGACGGG   4680

AAAGGACGTG GAAACAAGGC AGCAAAACGA GACCTTCCAC CAGCAAAGAC TCATCTCATC   4740

CAAGAGGATA TTCTACCTTA TTGTAGACCT ACTTTTCCAA CATCAAATAA TCCCAGAGAT   4800

CCCAGTTCCT CAAGCTCAAT GTCATCAAGA GGATCAGGAA GCAGACAAAG AGAACAAGCA   4860

AATGTAGGTC GAAGAAATAT TGCAGAAATG CAGGTACTTG GAGGATATGA AAGAGGAGAA   4920

GATAATAATG AAGAATTAGA GGAAACTGAA AGCTGA   4956

(2) INFORMATION FOR SEQ ID NO:8:
        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 1651 amino acids
             (B) TYPE: amino acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: peptide
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
       Met Lys Trp Lys His Val Pro Phe Leu Val Met Ile Ser Leu Leu Ser
       1   5   10   15
       Leu Ser Pro Asn His Leu Phe Leu Ala Gln Leu Ile Pro Asp Pro Glu
                       20   25   30
       Asp Val Glu Arg Gly Asn Asp His Gly Thr Pro Ile Pro Thr Ser Asp
                   35   40   45
       Asn Asp Asp Asn Ser Leu Gly Tyr Thr Gly Ser Arg Leu Arg Gln Glu

Asp Phe Pro Pro Arg Ile Val Glu His Pro Ser Asp Leu Ile Val Ser

65   70   75   80
Lys Gly Glu Pro Ala Thr Leu Asn Cys Lys Ala Glu Gly Arg Pro Thr

                85   90   95
Pro Thr Ile Glu Trp Tyr Lys Gly Gly Glu Arg Val Glu Thr Asp Lys

                100   105   110
Asp Asp Pro Arg Ser His Arg Met Leu Leu Pro Ser Gly Ser Leu Phe

        115   120   125
Phe Leu Arg Ile Val His Gly Arg Lys Ser Arg Pro Asp Glu Gly Val

        130   135   140
Tyr Val Cys Val Ala Arg Asn Tyr Leu Gly Glu Ala Val Ser His Asn

145   150   155   160
Ala Ser Leu Glu Val Ala Ile Leu Arg Asp Asp Phe Arg Gln Asn Pro

                165   170   175
Ser Asp Val Met Val Ala Val Gly Glu Pro Ala Val Met Glu Cys Gln

                180   185   190
Pro Pro Arg Gly His Pro Glu Pro Thr Ile Ser Trp Lys Lys Asp Gly

        195   200   205
Ser Pro Leu Asp Asp Lys Asp Glu Arg Ile Thr Ile Arg Gly Gly Lys

        210   215   220
Leu Met Ile Thr Tyr Thr Arg Lys Ser Asp Ala Gly Lys Tyr Val Cys

225   230   235   240
Val Gly Thr Asn Met Val Gly Glu Arg Glu Ser Glu Val Ala Glu Leu

                245   250   255
Thr Val Leu Glu Arg Pro Ser Phe Val Lys Arg Pro Ser Asn Leu Ala

                260   265   270
Val Thr Val Asp Asp Ser Ala Glu Phe Lys Cys Glu Ala Arg Gly Asp

        275   280   285
Pro Val Pro Thr Val Arg Trp Arg Lys Asp Asp Gly Glu Leu Pro Lys

        290   295   300
Ser Arg Tyr Glu Ile Arg Asp Asp His Thr Leu Lys Ile Arg Lys Val

305   310   315   320
Thr Ala Gly Asp Met Gly Ser Tyr Thr Cys Val Ala Glu Asn Met Val

                325   330   335
Gly Lys Ala Glu Ala Ser Ala Thr Leu Thr Val Gln Glu Pro Pro His

                340   345   350
Phe Val Val Lys Pro Arg Asp Gln Val Val Ala Leu Gly Arg Thr Val

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                355                   360                   365
Thr Phe Gln Cys Glu Ala Thr Gly Asn Pro Gln Pro Ala Ile Phe Trp
        370                   375                   380
Arg Arg Glu Gly Ser Gln Asn Leu Leu Phe Ser Tyr Gln Pro Pro Gln
385                   390                   395                   400
Ser Ser Ser Arg Phe Ser Val Ser Gln Thr Gly Asp Leu Thr Ile Thr
                405                   410                   415
Asn Val Gln Arg Ser Asp Val Gly Tyr Tyr Ile Cys Gln Thr Leu Asn
                420                   425                   430
Val Ala Gly Ser Ile Ile Thr Lys Ala Tyr Leu Glu Val Thr Asp Val
        435                   440                   445
Ile Ala Asp Arg Pro Pro Pro Val Ile Arg Gln Gly Pro Val Asn Gln
        450                   455                   460
Thr Val Ala Val Asp Gly Thr Phe Val Leu Ser Cys Val Ala Thr Gly
465                   470                   475                   480
Ser Pro Val Pro Thr Ile Leu Trp Arg Lys Asp Gly Val Leu Val Ser
                485                   490                   495
Thr Gln Asp Ser Arg Ile Lys Gln Leu Glu Asn Gly Val Leu Gln Ile
        500                   505                   510
Arg Tyr Ala Lys Leu Gly Asp Thr Gly Arg Tyr Thr Cys Ile Ala Ser
        515                   520                   525
Thr Pro Ser Gly Glu Ala Thr Trp Ser Ala Tyr Ile Glu Val Gln Glu
        530                   535                   540
Phe Gly Val Pro Val Gln Pro Pro Arg Pro Thr Asp Pro Asn Leu Ile
545                   550                   555                   560
Pro Ser Ala Pro Ser Lys Pro Glu Val Thr Asp Val Ser Arg Asn Thr
                565                   570                   575
Val Thr Leu Ser Trp Gln Pro Asn Leu Asn Ser Gly Ala Thr Pro Thr
                580                   585                   590
Ser Tyr Ile Ile Glu Ala Phe Ser His Ala Ser Gly Ser Ser Trp Gln
        595                   600                   605
Thr Val Ala Glu Asn Val Lys Thr Glu Thr Ser Ala Ile Lys Gly Leu
        610                   615                   620
Lys Pro Asn Ala Ile Tyr Leu Phe Leu Val Arg Ala Ala Asn Ala Tyr
625                   630                   635                   640
Gly Ile Ser Asp Pro Ser Gln Ile Ser Asp Pro Val Lys Thr Gln Asp
                645                   650                   655
Val Leu Pro Thr Ser Gln Gly Val Asp His Lys Gln Val Gln Arg Glu
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Leu Gly Asn Ala Val Leu His Leu His Asn Pro Thr Val Leu Ser Ser

Ser Ser Ile Glu Val His Trp Thr Val Asp Gln Gln Ser Gln Tyr Ile

Gln Gly Tyr Lys Ile Leu Tyr Arg Pro Ser Gly Ala Asn His Gly Glu

Ser Asp Trp Leu Val Phe Glu Val Arg Thr Pro Ala Lys Asn Ser Val

Val Ile Pro Asp Leu Arg Lys Gly Val Asn Tyr Glu Ile Lys Ala Arg

Pro Phe Phe Asn Glu Phe Gln Gly Ala Asp Ser Glu Ile Lys Phe Ala

Lys Thr Leu Glu Glu Ala Pro Ser Ala Pro Pro Gln Gly Val Thr Val

Ser Lys Asn Asp Gly Asn Gly Thr Ala Ile Leu Val Ser Trp Gln Pro

Pro Pro Glu Asp Thr Gln Asn Gly Met Val Gln Glu Tyr Lys Val Trp

Cys Leu Gly Asn Glu Thr Arg Tyr His Ile Asn Lys Thr Val Asp Gly

Ser Thr Phe Ser Val Val Ile Pro Phe Leu Val Pro Gly Ile Arg Tyr

Ser Val Glu Val Ala Ala Ser Thr Gly Ala Gly Ser Gly Val Lys Ser

Glu Pro Gln Phe Ile Gln Leu Asp Ala His Gly Asn Pro Val Ser Pro

Glu Asp Gln Val Ser Leu Ala Gln Gln Ile Ser Asp Val Val Lys Gln

Pro Ala Phe Ile Ala Gly Ile Gly Ala Ala Cys Trp Ile Ile Leu Met

Val Phe Ser Ile Trp Leu Tyr Arg His Arg Lys Lys Arg Asn Gly Leu

Thr Ser Thr Tyr Ala Gly Ile Arg Lys Val Pro Ser Phe Thr Phe Thr

Pro Thr Val Thr Tyr Gln Arg Gly Gly Glu Ala Val Ser Ser Gly Gly

Arg Pro Gly Leu Leu Asn Ile Ser Glu Pro Ala Ala Gln Pro Trp Leu

Ala Asp Thr Trp Pro Asn Thr Gly Asn Asn His Asn Asp Cys Ser Ile
         980   985   990

Ser Cys Cys Thr Ala Gly Asn Gly Asn Ser Asp Ser Asn Leu Thr Thr
       995   1000   1005

Tyr Ser Arg Pro Ala Asp Cys Ile Ala Asn Tyr Asn Asn Gln Leu Asp
   1010   1015   1020

Asn Lys Gln Thr Asn Leu Met Leu Pro Glu Ser Thr Val Tyr Gly Asp
1025   1030   1035   1040

Val Asp Leu Ser Asn Lys Ile Asn Glu Met Lys Thr Phe Asn Ser Pro
      1045   1050   1055

Asn Leu Lys Asp Gly Arg Phe Val Asn Pro Ser Gly Gln Pro Thr Pro
       1060   1065   1070

Tyr Ala Thr Thr Gln Leu Ile Gln Ser Asn Leu Ser Asn Asn Met Asn
      1075   1080   1085

Asn Gly Ser Gly Asp Ser Gly Glu Lys His Trp Lys Pro Leu Gly Gln
   1090   1095   1100

Gln Lys Gln Glu Val Ala Pro Val Gln Tyr Asn Ile Val Glu Gln Asn
1105   1110   1115   1120

Lys Leu Asn Lys Asp Tyr Arg Ala Asn Asp Thr Val Pro Pro Thr Ile
      1125   1130   1135

Pro Tyr Asn Gln Ser Tyr Asp Gln Asn Thr Gly Gly Ser Tyr Asn Ser
      1140   1145   1150

Ser Asp Arg Gly Ser Ser Thr Ser Gly Ser Gln Gly His Lys Lys Gly
      1155   1160   1165

Ala Arg Thr Pro Lys Val Pro Lys Gln Gly Gly Met Asn Trp Ala Asp
   1170   1175   1180

Leu Leu Pro Pro Pro Pro Ala His Pro Pro His Ser Asn Ser Glu
1185   1190   1195   1200

Glu Tyr Asn Ile Ser Val Asp Glu Ser Tyr Asp Gln Glu Met Pro Cys
      1205   1210   1215

Pro Val Pro Pro Ala Arg Met Tyr Leu Gln Gln Asp Glu Leu Glu Glu
      1220   1225   1230

Glu Glu Asp Glu Arg Gly Pro Thr Pro Pro Val Arg Gly Ala Ala Ser
      1235   1240   1245

Ser Pro Ala Ala Val Ser Tyr Ser His Gln Ser Thr Ala Thr Leu Thr
      1250   1255   1260

Pro Ser Pro Gln Glu Glu Leu Gln Pro Met Leu Gln Asp Cys Pro Glu

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        1265                  1270                  1275                  1280
Glu Thr Gly His Met Gln His Gln Pro Asp Arg Arg Arg Gln Pro Val
                  1285                  1290                  1295
Ser Pro Pro Pro Pro Pro Arg Pro Ile Ser Pro Pro His Thr Tyr Gly
                  1300                  1305                  1310
Tyr Ile Ser Gly Pro Leu Val Ser Asp Met Asp Thr Asp Ala Pro Glu
                  1315                  1320                  1325
Glu Glu Glu Asp Glu Ala Asp Met Glu Val Ala Lys Met Gln Thr Arg
             1330                  1335                  1340
Arg Leu Leu Leu Arg Gly Leu Glu Gln Thr Pro Ala Ser Ser Val Gly
1345                  1350                  1355                  1360
Asp Leu Glu Ser Ser Val Thr Gly Ser Met Ile Asn Gly Trp Gly Ser
                  1365                  1370                  1375
Ala Ser Glu Glu Asp Asn Ile Ser Ser Gly Arg Ser Ser Val Ser Ser
                  1380                  1385                  1390
Ser Asp Gly Ser Phe Phe Thr Asp Ala Asp Phe Ala Gln Ala Val Ala
             1395                  1400                  1405
Ala Ala Ala Glu Tyr Ala Gly Leu Lys Val Ala Arg Arg Gln Met Gln
             1410                  1415                  1420
Asp Ala Ala Gly Arg Arg His Phe His Ala Ser Gln Cys Pro Arg Pro
1425                  1430                  1435                  1440
Thr Ser Pro Val Ser Thr Asp Ser Asn Met Ser Ala Ala Val Met Gln
                  1445                  1450                  1455
Lys Thr Arg Pro Ala Lys Lys Leu Lys His Gln Pro Gly His Leu Arg
                  1460                  1465                  1470
Arg Glu Thr Tyr Thr Asp Asp Leu Pro Pro Pro Val Pro Pro Pro
             1475                  1480                  1485
Ala Ile Lys Ser Pro Thr Ala Gln Ser Lys Thr Gln Leu Glu Val Arg
             1490                  1495                  1500
Pro Val Val Val Pro Lys Leu Pro Ser Met Asp Ala Arg Thr Asp Arg
1505                  1510                  1515                  1520
Ser Ser Asp Arg Lys Gly Ser Ser Tyr Lys Gly Arg Glu Val Leu Asp
                  1525                  1530                  1535
Gly Arg Gln Val Val Asp Met Arg Thr Asn Pro Gly Asp Pro Arg Glu
                  1540                  1545                  1550
Ala Gln Glu Gln Gln Asn Asp Gly Lys Gly Arg Gly Asn Lys Ala Ala
             1555                  1560                  1565
Lys Arg Asp Leu Pro Pro Ala Lys Thr His Leu Ile Gln Glu Asp Ile
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              1570                    1575                    1580
      Leu Pro Tyr Cys Arg Pro Thr Phe Pro Thr Ser Asn Asn Pro Arg Asp
      1585                    1590                    1595                    1600
      Pro Ser Ser Ser Ser Ser Met Ser Ser Arg Gly Ser Gly Ser Arg Gln
                        1605                    1610                    1615
      Arg Glu Gln Ala Asn Val Gly Arg Arg Asn Ile Ala Glu Met Gln Val
                        1620                    1625                    1630
      Leu Gly Gly Tyr Glu Arg Gly Glu Asp Asn Asn Glu Glu Leu Glu Glu
                  1635                    1640                    1645
      Thr Glu Ser
            1650
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(2) INFORMATION FOR SEQ ID NO:9:

   (i) SEQUENCE CHARACTERISTICS:

      (A) LENGTH: 1300 base pairs

      (B) TYPE: nucleic acid

      (C) STRANDEDNESS: double

      (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: cDNA

   (ix) FEATURE:

      (A) NAME/KEY: misc_feature

      (B) LOCATION: 855..1187

      (D) OTHER INFORMATION: /note= "N signifies gap in sequence"

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
CAGATTGTTG CTCAAGGTCG AACAGTGACA TTTCCCTGTG AAACTAAAGG AAACCCACAG      60
CCAGCTGTTT TTTGGCAGAA AGAAGGCAGC CAGAACCTAC TTTTCCCAAA CCAACCCCAG     120
CAGCCCAACA GTAGATGCTC AGTGTCACCA ACTGGAGACC TCACAATCAC CAACATTCAA     180
CGTTCCGACG CGGGTTACTA CATCTGCCAG GCTTTAACTG TGGCAGGAAG CATTTTAGCA     240
AAAGCTCAAC TGGAGGTTAC TGATGTTTTG ACAGATAGAC CTCCACCTAT AATTCTACAA     300
GGCCCAGCCA ACCAAACGCT GGCAGTGGAT GGTACAGCGT TACTGAAATG TAAAGCCACT     360
GGTGATCCTC TTCCTGTAAT TAGCTGGTTA AAGGAGGGAT TTACTTTTCC GGGTAGAGAT     420
CCAAGAGCAA CAATTCAAGA GCAAGGCACA CTGCAGATTA AGAATTTACG GATTTCTGAT     480
ACTGGCACTT ATACTTGTGT GGCTACAAGT TCAAGTGGAG AGGCTTCCTG GAGTGCAGTG     540
CTGGATGTGA CAGAGTCTGG AGCAACAATC AGTAAAAACT ATGATTTAAG TGACCTGCCA     600
GGGCCACCAT CCAAACCGCA AGTCACTGAT GTTACTAAGA ACAGTGTCAC CTTGTCCTGG     660
CAGCCAGGTA CCCCTGGAAC CCTTCCAGCA AGTGCATATA TCATTGAGGC TTTCAGCCAA     720
TCAGTGAGCA ACAGCTGGCA GACCGTGGCA AACCATGTAA AGACCACCCT CTATACTGTA     780
AGAGGACTGC GGCCCAATAC AATCTACTTA TTCATGGTCA GAGCGATCAA CCCCAAGGTY     840
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TCAGTGACCC AAGTNAAACC ACAGAAAAAC AATGGATCCA CTTGGGCCAA TGTCCCTCTA   900

CCTCCCCCCC CAGTCCAGCC CCTTCCTGGC ACGGAGCTGG AACACTATGC AGTGGAACAA   960

CAAGAAAATG GCTATGACAG TGATAGCTGG TGCCCACCAT TGCCAGTACA AACTTACTTA   1020

CACCAAGGTC TGGAAGATGA ACTGGAAGAA GATGATGATA GGGTCCCAAC ACCTCCTGTT   1080

CGAGGCGTGG CTTCTTCTCC TGCTATCTCC TTTGGACAGC AGTCCACTGC AACTCTTACT   1140

CCATCCCCAC GGGAAGAGAT GCAACCCATG CTGCAGGCTT CACCTNTTTA CCTCCTCTCA   1200

AAGACCTCGA CCTACCAGCC CATTTTCTAC TGACAGTAAC ACCAGTGCAG CCCTGAGTCA   1260

AAGTCAGAGG CCTCGGCCCA CTAAAAAACA CAAGGGAGGG   1300

(2) INFORMATION FOR SEQ ID NO:10:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 434 amino acids

        (B) TYPE: amino acid

        (C) STRANDEDNESS: single

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (ix) FEATURE:

        (A) NAME/KEY: Modified-site

        (B) LOCATION: 285..396

        (D) OTHER INFORMATION: /note= "Xaa signifies gap in sequence"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gln Ile Val Ala Gln Gly Arg Thr Val Thr Phe Pro Cys Glu Thr Lys
1   5   10   15

Gly Asn Pro Gln Pro Ala Val Phe Trp Gln Lys Glu Gly Ser Gln Asn
         20   25   30

Leu Leu Phe Pro Asn Gln Pro Gln Gln Pro Asn Ser Arg Cys Ser Val
         35   40   45

Ser Pro Thr Gly Asp Leu Thr Ile Thr Asn Ile Gln Arg Ser Asp Ala
         50   55   60

Gly Tyr Tyr Ile Cys Gln Ala Leu Thr Val Ala Gly Ser Ile Leu Ala
65   70   75   80

Lys Ala Gln Leu Glu Val Thr Asp Val Leu Thr Asp Arg Pro Pro Pro
         85   90   95

Ile Ile Leu Gln Gly Pro Ala Asn Gln Thr Leu Ala Val Asp Gly Thr
         100   105   110

Ala Leu Leu Lys Cys Lys Ala Thr Gly Asp Pro Leu Pro Val Ile Ser
         115   120   125

Trp Leu Lys Glu Gly Phe Thr Phe Pro Gly Arg Asp Pro Arg Ala Thr

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            130                    135                    140
Ile Gln Glu Gln Gly Thr Leu Gln Ile Lys Asn Leu Arg Ile Ser Asp
145                    150                    155                    160
Thr Gly Thr Tyr Thr Cys Val Ala Thr Ser Ser Ser Gly Glu Ala Ser
                      165                    170                    175
Trp Ser Ala Val Leu Asp Val Thr Glu Ser Gly Ala Thr Ile Ser Lys
                      180                    185                    190
Asn Tyr Asp Leu Ser Asp Leu Pro Gly Pro Pro Ser Lys Pro Gln Val
                      195                    200                    205
Thr Asp Val Thr Lys Asn Ser Val Thr Leu Ser Trp Gln Pro Gly Thr
            210                    215                    220
Pro Gly Thr Leu Pro Ala Ser Ala Tyr Ile Ile Glu Ala Phe Ser Gln
225                    230                    235                    240
Ser Val Ser Asn Ser Trp Gln Thr Val Ala Asn His Val Lys Thr Thr
                      245                    250                    255
Leu Tyr Thr Val Arg Gly Leu Arg Pro Asn Thr Ile Tyr Leu Phe Met
                      260                    265                    270
Val Arg Ala Ile Asn Pro Lys Val Ser Val Thr Gln Xaa Lys Pro Gln
                      275                    280                    285
Lys Asn Asn Gly Ser Thr Trp Ala Asn Val Pro Leu Pro Pro Pro Pro
            290                    295                    300
Val Gln Pro Leu Pro Gly Thr Glu Leu Glu His Tyr Ala Val Glu Gln
305                    310                    315                    320
Gln Glu Asn Gly Tyr Asp Ser Asp Ser Trp Cys Pro Pro Leu Pro Val
                      325                    330                    335
Gln Thr Tyr Leu His Gln Gly Leu Glu Asp Glu Leu Glu Glu Asp Asp
                      340                    345                    350
Asp Arg Val Pro Thr Pro Pro Val Arg Gly Val Ala Ser Ser Pro Ala
            355                    360                    365
Ile Ser Phe Gly Gln Gln Ser Thr Ala Thr Leu Thr Pro Ser Pro Arg
            370                    375                    380
Glu Glu Met Gln Pro Met Leu Gln Ala Ser Pro Xaa Phe Thr Ser Ser
385                    390                    395                    400
Gln Arg Pro Arg Pro Thr Ser Pro Phe Ser Thr Asp Ser Asn Thr Ser
                      405                    410                    415
Ala Ala Leu Ser Gln Ser Gln Arg Pro Arg Pro Thr Lys Lys His Lys
                      420                    425                    430
Gly Gly
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(2) INFORMATION FOR SEQ ID NO:11:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 444 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: double

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

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GCCCAGGCAG TTGCTGCAGC TGCGGAGTAT GCGGGCCTGA AAGTGGCTCG CCGCCAAATG      60
CAAGATGCTG CTGGCCGCCG CCACTTCCAT GCCTCTCAGT GCCCAAGGCC CACGAGTCCT     120
GTGTCCACAG ACAGCAACAT GAGTGCTGTT GTGATCCAGA AAGCCAGACC CGCCAAGAAG     180
CAGAAACACC AGCCAGGACA TCTGCGCAGG GAAGCCTACG CAGATGATCT TCCACCCCCT     240
CCAGTGCCAC CACCTGCTAT AAAATCGCCC ACTGTCCAGT CCAAGGCACA GCTGGAGGTA     300
CGGCCTGTCA TGGTGCCAAA ACTCGCGTCT ATAGAAGCAA GGACAGATAG ATCGTCAGAC     360
AGAAAAGGAG GCAGTTACAA GGGGAGAGAA GCTCTGGATG GAAGACAAGT CACTGACCTG     420
CGAACAAATC CAAGTGACCC CAGA                                           444
```

(2) INFORMATION FOR SEQ ID NO:12:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 148 amino acids

        (B) TYPE: amino acid

        (C) STRANDEDNESS: single

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
Ala Gln Ala Val Ala Ala Ala Ala Glu Tyr Ala Gly Leu Lys Val Ala
1               5                   10                  15
Arg Arg Gln Met Gln Asp Ala Ala Gly Arg Arg His Phe His Ala Ser
            20                  25                  30
Gln Cys Pro Arg Pro Thr Ser Pro Val Ser Thr Asp Ser Asn Met Ser
            35                  40                  45
Ala Val Val Ile Gln Lys Ala Arg Pro Ala Lys Lys Gln Lys His Gln
        50                  55                  60
Pro Gly His Leu Arg Arg Glu Ala Tyr Ala Asp Asp Leu Pro Pro Pro
65                  70                  75                  80
Pro Val Pro Pro Pro Ala Ile Lys Ser Pro Thr Val Gln Ser Lys Ala
                85                  90                  95
```

```
Gln Leu Glu Val Arg Pro Val Met Val Pro Lys Leu Ala Ser Ile Glu
            100                 105                 110
Ala Arg Thr Asp Arg Ser Ser Asp Arg Lys Gly Gly Ser Tyr Lys Gly
            115                 120                 125
Arg Glu Ala Leu Asp Gly Arg Gln Val Thr Asp Leu Arg Thr Asn Pro
    130                 135                 140
Ser Asp Pro Arg
145
```